PCysM1:
5'ATATGGATCCATCGAGGGTAGGGCCGATGCCGGCTACGCCCCGGC
CACCCCGGCTGCATGCGGAGCG-3' (SEQ ID NO 98)

Please amend the paragraph on page 33, lines 19 through 25 as follows:

Plasmid pGS21 (see above) was used as the starting vector for cloning the deletion mutant DM1. The bp 399 -1374 fragment of the cDNA for rPh1 p 5b was amplified in a PCR using the following primers:

MP2 sense:
5'-GCTAGCCGGCGAGCTGCAGATCATCG-3' (SEQ ID NO 99)

REMARKS

The above amendment is submitted in response to the Notice of Non-Compliant Amendment mailed September 20, 2001. No new matter is introduced and it is respectfully requested that the application be examined on its merits.

Respectfully submitted,

Nancy J. Axelrod
Registration No. 44,014
Attorney for Applicant(s)

MILLEN, WHITE, ZELANO, & BRANIGAN, P.C.
Arlington Courthouse Plaza I, Suite 1400
2200 Clarendon Boulevard
Arlington, Virginia 22201
Telephone: (703) 243-6333
Facsimile: (703) 243-6410

Attorney Docket No.: MERCK-2034
Filed: October 22, 2001

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Please amend pages 6, 9-11, 28 and 31-33 as follows:

Please amend the paragraph beginning on page 5, line 26, through page 6, line 12 as follows:

Using the single-letter code for amino acids, the sequence of Phl p 5b is as follows:

ADAGYAPATPAAAGAAAGKATTEEQKLIEDINVGFKAAVAAAASVPAADK

1 10 20 30 40 50

FKTFEAAFTSSSKAAAAKAPGLVPKLDAAYSVAYKAAVGATPEAKFDSFV

51 60 70 80 90 100

ASLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAA

101 110 120 130 140 150

TAAATAPADDKFTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQAYAA

151 160 170 180 190 200

TVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAG

201 210 220 230 240 250

AASGAATVAAGGYKV (SEQ ID NO 87)

251 260 265

Please amend the paragraph on page 9, lines 1-9 as follows:

In this context, PM1 denotes point mutation 1 and has the following sequence (the amino acids which are replaced as compared with Phl p 5b are printed in bold):

ADAGYAPATPAAAGAAAGKATTEEQKLIEDIDVGFKAAVAAAASVPAALA

1 10 20 30 40 50

FKTFEAAFTSSSKAAAAKAPGLVPKLDAAYSVAYKAAVGATPEAKFDSFV

51 60 70 80 90 100

ASLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAA

101 110 120 130 140 150

TAAATAPADDKFTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQAYAA

151 160 170 180 190 200

TVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAG

201 210 220 230 240 250

AASGAATVAAGGYKV (SEQ ID NO 88)

251 260 265

Please amend the paragraphs beginning on page 9, line 10 through page 10, line 16 as follows:

The other particularly preferred peptides have the following sequences:

PM2 ($D^{49} \rightarrow L$, $K^{50} \rightarrow A$):

ADAGYAPATPAAAGAAAGKATTEEQKLIEDINVGFKAAVAAAASVPAALA

1 10 20 30 40 50

FKTFEAAFTSSSKAAAAAKAPGLVPKLDAAYSVAYKAAVGATPEAKFDSFV

51 60 70 80 90 100

ASLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAA

101 110 120 130 140 150

TAAATAPADDKFTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQAYAA

151 160 170 180 190 200

TVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAG

201 210 220 230 240 250

AASGAATVAAGGYKV (SEQ ID NO 89)

251 260 265

DM3 ($\Delta^{33} \rightarrow C$):

ADAGYAPATPAACGAAAGKATTEEQKLIEDINVGFKAAVAAAASVPAADK

1 10 20 30 40 50

FKTFEAAFTSSSKAAAAKAPGLVPKLDAAYSVAYKAAVGATPEAKFDSFV

51 60 70 80 90 100

ASLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAA

101 110 120 130 140 150

TAAATAPADDKFTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQAYAA

151 160 170 180 190 200

TVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAG

201 210 220 230 240 250

AASGAATVAAGGYKV (SEQ ID NO 90)

251 260 265

DM1 ($\Delta\ K^{30} \rightarrow P^{\Delta 132}$, $D^{49} \rightarrow L$):

ADAGYAPATPAAAGAAAGKATTEEQKLIEDINVGFKAAVAAAASVPAALA

1 10 20 30 40 50

GELQIIDKIDAAFKVAATAAATAPADDKFTVFEAAFNKAIKESTGGAYDTYK

51 60 70 80 90 100

CIPSLEAAVKQAYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATG

103 110 120 130 140 150

AATVAAGAATTAAGAASGAATVAAGGYKV (SEQ ID NO 91)

154 160 170 180

DM 2 ($\Delta\ F^{31} - G^{178}$, $D^{49} - L$, $K^{30} - A$):

ADAGYAPATPAAAGAAAGKATTEEQKLIEDINVGFKAAVAAAASVPAALA

1 10 20 30 40 50

GAYDTYKCIPSLEAAVKQAYAATVAAAPQVKYAVFEAALTKAITAMSEVQK

51 60 70 80 90 100

VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV (SEQ ID NO 92)

102 110 120 130 137

Please amend the paragraph on page 11, lines 2 through lines 12 as follows:

This sequence corresponds to that of DM2 where, however, the amino acids of positions 179-217 of the starting peptide Ph1 p 5b additionally exhibit an altered sequence and all the subsequent amino acids are missing.

DM3 (Δ A^{154} - T^{177}, $A^{220} \rightarrow T$):

ADAGYAPATPAAAGAAAGKATTEEQKLIEDINVGFKAAVAAAASVPAADK

1 10 20 30 40 50

FKTFEAAFTSSSKAAAAKAPGLVPKLDAAYSVAYKAAVGATPEAKFDSFV

51 60 70 80 90 100

ASLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAA

101 110 120 130 140 150

TAAGGAYDTYKCIPSLEAAVKQAYAATVAAAPQVKYAVFEAALTKTITAMS

151 160 170 180 190 200

EVQKVSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV (SEQ ID NO 93)

202 210 220 230 240

Please amend the paragraph on page 28, lines 3 through lines 48 as follows:

Tab. 1: Dodecapeptides which are based n the Ph1 p 5b sequence and which are used for determining the T cell-reactive regions

1	ADAGYAPATPAA	(SEQ ID NO 1)	44	KIPAGELQIIDK	(SEQ ID NO 44)
2	GYAPATPAAAGA	(SEQ ID NO 2)	45	AGELQIIDKIDA	(SEQ ID NO 45)
3	PATPAAAGAAAG	(SEQ ID NO 3)	46	LQIIDKIDAAFK	(SEQ ID NO 46)
4	PAAAGAAAGKAT	(SEQ ID NO 4)	47	IDKIDAAFKVAA	(SEQ ID NO 47)
5	AGAAAGKATTEE	(SEQ ID NO 5)	48	IDAAFKVAATAA	(SEQ ID NO 48)
6	AAGKATTEEQKL	(SEQ ID NO 6)	49	AFKVAATAAATA	(SEQ ID NO 49)
7	KATTEEQKLIED	(SEQ ID NO 7)	50	VAATAAATAPAD	(SEQ ID NO 50)
8	TEEQKLIEDINV	(SEQ ID NO 8)	51	TAAATAPADDKF	(SEQ ID NO 51)
9	QKLIEDINVGFK	(SEQ ID NO 9)	52	ATAPADDKFTVF	(SEQ ID NO 52)
10	IEDINVGFKAAV	(SEQ ID NO 10)	53	PADDKFTVFEAA	(SEQ ID NO 53)
11	INVGFKAAVAAA	(SEQ ID NO 11)	54	DKFTVFEAAFNK	(SEQ ID NO 54)
12	GFKAAVAAAASV	(SEQ ID NO 12)	55	TVFEAAFNKAIK	(SEQ ID NO 55)
13	AAVAAAASVPAA	(SEQ ID NO 13)	56	EAAFNKAIKEST	(SEQ ID NO 56)
14	AAAASVPAADKF	(SEQ ID NO 14)	57	FNKAIKESTGGA	(SEQ ID NO 57)
15	ASVPAADKFKTF	(SEQ ID NO 15)	58	AIKESTGGAYDT	(SEQ ID NO 58)
16	PAADKFKTFEAA	(SEQ ID NO 16)	59	ESTGGAYDTYKC	(SEQ ID NO 59)
17	DKFKTFEAAFTS	(SEQ ID NO 17)	60	GGAYDTYKCIPS	(SEQ ID NO 60)
18	KTFEAAFTSSSK	(SEQ ID NO 18)	61	YDTYKCIPSLEA	(SEQ ID NO 61)
19	EAAFTSSSKAAA	(SEQ ID NO 19)	62	YKCIPSLEAAVK	(SEQ ID NO 62)
20	FTSSSKAAAAKA	(SEQ ID NO 20)	63	IPSLEAAVKQAY	(SEQ ID NO 63)
21	SSKAAAAKAPGL	(SEQ ID NO 21)	64	LEAAVKQAYAAT	(SEQ ID NO 64)
22	AAAAKAPGLVPK	(SEQ ID NO 22)	65	AVKQYAATYAA	(SEQ ID NO 65)
23	AKAPGLVPKLDA	(SEQ ID NO 23)	66	QAYAATVAAAPQ	(SEQ ID NO 66)
24	PGLVPKLDAAYS	(SEQ ID NO 24)	67	AATVAAAPQVKY	(SEQ ID NO 67)
25	VPKLDAAYSVAY	(SEQ ID NO 25)	68	VAAAPQVKYAVF	(SEQ ID NO 68)
26	LDAAYSVAYKAA	(SEQ ID NO 26)	69	APQVKYAVFEAA	(SEQ ID NO 69)
27	AYSVAYKAAVGA	(SEQ ID NO 27)	70	VKYAVFEAALTK	(SEQ ID NO 70)
28	VAYKAAVGATPE	(SEQ ID NO 28)	71	AVFEAALTKAIT	(SEQ ID NO 71)
29	KAAVGATPEAKF	(SEQ ID NO 29)	72	EAALTKAITAMS	(SEQ ID NO 72)
30	VGATPEAKFDSF	(SEQ ID NO 30)	73	LTKAITAMSEVQ	(SEQ ID NO 73)
31	TPEAKFDSFVAS	(SEQ ID NO 31)	74	AITAMSEVQKVS	(SEQ ID NO 74)
32	AKFDSFVASLTE	(SEQ ID NO 32)	75	AMSEVQKVSQPA	(SEQ ID NO 75)
33	DSFVASLTEALR	(SEQ ID NO 33)	76	EVQKVSQPATGA	(SEQ ID NO 76)
34	VASLTEALRVIA	(SEQ ID NO 34)	77	KVSQPATGAATV	(SEQ ID NO 77)
35	LTEALRVIAGAL	(SEQ ID NO 35)	78	QPATGAATVAAG	(SEQ ID NO 78)
36	ALRVIAGALEVH	(SEQ ID NO 36)	79	TGAATVAAGAAT	(SEQ ID NO 79)
37	VIAGALEVHAVK	(SEQ ID NO 37)	80	ATVAAGAATTAA	(SEQ ID NO 80)
38	GALEVHAVKPVT	(SEQ ID NO 38)	81	AAGAATTAAGAA	(SEQ ID NO 81)
39	EVHAVKPVTEEP	(SEQ ID NO 39)	82	AATTAAGAASGA	(SEQ ID NO 82)
40	AVKPVTEEPGMA	(SEQ ID NO 40)	83	TAAGAASGAATV	(SEQ ID NO 83)
41	PVTEEPGMAKIP	(SEQ ID NO 41)	84	GAASGAATVAAG	(SEQ ID NO 84)
42	EEPGMAKIPAGE	(SEQ ID NO 42)	85	SGAATVAAGGYK	(SEQ ID NO 85)
43	GMAKIPAGELQI	(SEQ ID NO 43)	86	GAATVAAGGYKV	(SEQ ID NO 86)

Please amend the paragraph on page 31, lines 35 through page 32, lines 7 as follows:

Fragment 1:

Ph1 p 5b sense:

5'-ATATGGATCCATCGAGGGAAGGGCCGATGCCGGCTACGCC-3' (SEQ ID NO 94)

MP1 antisense:

5'-GAACGCTAGCGCCGCAGGGACGCTGGC-3' (SEQ ID NO 95)

Fragment 2:

MP1 sense:

5'-GCGCTAGCGTTCAAGACCTTCGAG-3' (SEQ ID NO 96)

Ph1 p 5b antisense:

5'-ATATAAGCTTTCCTCTGAAGGAAGGCAACCC-3' (SEQ ID NO 97)

Please amend the paragraph on page 32, lines 30-38 as follows:

The point mutant rPh1 p 5b PM1 was prepared in analogy with PM2. It contains, as the result of a PCR error, an additional point mutation: $N^{32} \rightarrow D$.

In order to clone this point mutant, the entire cDNA for rPh1 p 5b in vector pGS13 was amplified in a PCR using the following primers.

PCysM1:

5'ATATGGATCCATCGAGGGTAGGGCCGATGCCGGCTACGCCCCGGC
CACCCCGGCTGCATGCGGAGCG-3' (SEQ ID NO 98)

Please amend the paragraph on page 33, lines 19 through 25 as follows:

Plasmid pGS21 (see above) was used as the starting vector for cloning the deletion mutant DM1. The bp 399 -1374 fragment of the cDNA for rPh1 p 5b was amplified in a PCR using the following primers:

MP2 sense:

5'-GCTAGCCGGCGAGCTGCAGATCATCG-3' (SEQ ID NO 99)